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Modeling and simulation of Classical Swine Fever Virus spread between and within farms

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Abstract

Classical swine fever is a viral disease of pigs that causes severe commercial restrictions to the affected areas. The knowledge of its spread patterns and risk factors would help to implement specific measures for controlling future outbreaks. In this article, we introduce a spatial hybrid model, based on the combination of a stochastic individual based model for between-farm spread with a Susceptible-Infected model for within-farm spread, to simulate the spread of this disease in a given region. Then, this model is validated by comparing the results given by numerical experiments considering the Spanish province of Segovia with other studies based on real outbreaks. Finally, a brief sensitivity analysis of the model parameters is performed.

keywords: Classical swine fever; Epidemiological model; Individual based model; Susceptible-Infected model

1 Introduction

Modeling and simulation are important tools to fight diseases [2]. Each disease has its own characteristics and, therefore, most of them need a well-adapted

mathematical model in order to be able to tackle real-life situations [4].

In this article, we consider the Classical Swine Fever (CSF). CSF is a highly contagious viral disease of domestic and wild pigs caused by the Classical Swine Fever Virus (CSFV) [28]. It generates important economical losses (as infected pigs cannot be commercialized [39]) in the affected regions [17, 29, 34]. Despite the efforts to control and eradicate CSF, this disease remains endemic in many countries of America, Africa and Asia and sporadic outbreaks have been affecting half of the European countries from 1996 to 2007 [10, 9, 31, 32]. Due to the different ways of CSFV spread (airbornes, contact with infected animals, etc.) [5, 9, 20, 33], it is difficult to extrapolate the routes of infection and consequences of a CSF epidemic from one region to another. Furthermore, the magnitude and duration of a CSF epidemic change depending on the epidemiological and demographic characteristics of the infected region and the timing and effectiveness of the control measures applied [14, 18, 38].

The study of the potential spread patterns of CSFV into a region may help to identify risk areas to improve the prevention and management of future outbreaks. In CSF-free areas, a good way to quantify the magnitude of potential CSF epidemics and evaluate the efficiency of different control measures is to use mathematical models. Recently, some models have been developed to simulate CSFV spread into CSF-free regions such as Belgium, Germany, Australia and Netherlands [12, 14, 16, 36, 37]. Martinez et al., [25] also have described a spatial stochastic model for Spain by using a commercial available software (InterSpread Plus [35]). However, most of those models only focus on the between-farm spread of the CSFV, with poor assumptions regarding the within-farm spread and do not explicitly consider the specific farm to farm contact patterns into the studied region.

The work, presented here, intends to provide quantitative estimates of the magnitude and duration of potential CSF-epidemics by considering a spatial hybrid model to simulate both within-farm and between-farm spreads. This model is based on the combination of a stochastic individual based model [6, 14], modeling the between-farm spread, with a Susceptible-Infected model [4, 16], modeling the within-farm spread. In order to validate this model, we consider various numerical experiments, using a real database provided by the "Regional Government of Castilla and Leon" [13] and the Spanish "Ministry of the Environment and Rural and Marine Affairs" [27], and compare their given results with those obtained in other works based on numerical or experimental studies of CSF outbreaks [3, 5, 15, 35, 37]. Finally, we perform a brief sensitivity analysis of the model parameters in order to check its robustness. All those experiments are based on a particular Matlab implementation of this model, called *Be-FAST* (Between-Farm-Animal Spatial Transmission) [22].

2 Classical Swine Fever characteristics

In order to help in the understanding of the model described in Section 3, we explain briefly the main characteristics of the CSF, recall some basic definitions

in epidemiology and present some control measures used to fight CSFV. All those concepts have to be taken into account when developing the model.

CSF results from infection by CSFV, a member of the genus Pestivirus and family Flaviviridae [28]. CSFV affects both domestic and wild pigs. When a pig is not infected by CSFV, it is categorized in the 'Susceptible' state (denoted by S_p). Once it is infected, it will pass successively through the following states [29, 30]:

- 'Infected' (denoted by I_p): The pig is infected by CSFV but cannot infect other pigs and have no visible clinical signs (fever, lesion, etc.). The mean duration of a pig in this state is 7 days and it is called 'latent' period. Then, it passes to be infectious.
- 'Infectious': The pig can infect other pigs but does not have clinical signs yet. The mean duration from infectious to the development of clinical sign is 21 days and it is called 'incubation' period. Then, the pig has clinical signs.
- 'Clinical signs': The pig develops visible clinical signs. After a period between two weeks and three months the pig can be recovered or died due to the disease. The CSF death of pigs is assumed to be neglected, because the time period considered in our simulation is short (\leq one year) and the slaughter of infected animals is considered.

Those four states can be also applied at the farm level by considering [14]:

- 'Susceptible' (denoted by S_f): If none of the pigs in the farm are infected.
- 'Infected' (denoted by I_f): If at least one pig is infected.
- 'Infectious' (denoted by T_f): If at least one pig is infectious.
- 'Clinical Signs' (denoted by C_f): If at least one pig has clinical signs.

A farm in the state I_f , T_f or C_f is called 'Contaminated' farm.

The main ways of CSFV spread (i.e., that a susceptible pig becomes infected) are the following [5, 9, 20, 33]:

- By contact with an infected animal. This way of spreading is called 'direct contact'. By definition, all the other ways of spreading are called 'indirect contacts'.
- By contact with contaminated material (such as, fomite, vehicles, etc.) or people (in particular, veterinarians, visitors or neighborhood farmers).
- By airborne spread.

Historically, those ways of spreading have been reported as the main routes of CSFV spread [7], although other routes (such as, movement of wild animals) have also been described as potential ways of spreading [9]. Those alternative routes have been neglected here.

Once an animal becomes infected, another important concept in epidemiology is its detection by the authorities [29]. When an infected pig is detected in a farm, this farm is classified as 'Detected'. Generally, in a zone free of CSFV (i.e., before the detection of the first infected farm, called 'index case'), the detection occurs when pigs present clinical signs and is due to the awareness of the own farmers [18]. When the first farm is detected, the awareness of the farmers and authorities is widely increased and the detection delay decrease [14, 36]. Moreover, the detection can be also due to the control measures presented below.

Finally, in order to control a potential CSF epidemic, some measures defined by the European and Spanish legislation [12, 13, 19, 21] are considered here:

- Zoning: Zones (called 'control' and 'surveillance' zones) are defined around a detected farm, and movement restrictions and surveillance activities are applied with-in those zones during a fixed time period.
- Movement restrictions: All movements inside the considered region are limited during a specified time interval.
- Depopulation: All the animals of a detected farm are slaughtered.
- Tracing: Tracing activities involve the process of identifying contacts that have left or entered a detected farm during a time interval preceding the detection. The objective of tracing is to identify potentially infectious contacts which may have introduced CSFV into the farm or spread CSFV to other farms.

3 Model description

3.1 General description

A spatial hybrid model, referred as **CSM** (CSF Spread Model), is developed to evaluate the daily spread of CSFV within and between farms into a specific region.

At the beginning of the simulation, the model parameters are set by the user. Those referring to farms and transport of pigs are described in detail in Section 3.2, the other ones in the following sections. Furthermore, control measures, presented in Section 2, are also implemented and can be activated/deactivated at the beginning of the simulation in order to quantify their effectiveness to reduce the magnitude and duration of the epidemic.

CSM is based on a Monte Carlo approach that generates $M \in \mathbb{N}$ possible epidemic scenarios (i.e., evolution of the CSFV). More precisely:

At the beginning of each scenario (i.e., at time $t = 0$), denoted by (SCE_m) , $m = 1, 2, \dots, M$, all farms are in the susceptible state (i.e., pigs are free of CSFV) except one randomly selected farm, which is assumed to have one infectious pig and is classified as infectious. Then, during a time interval $[0, T]$, with $T \in \mathbb{N}$ a maximum simulation day number, the within-farm and between-farm daily spread processes, described in Sections 3.3 and 3.4 respectively, are applied. A daily process simulating the detection of contaminated farms by authorities and a daily process modeling the activated control measures, presented in Sections 3.5 and 3.6 respectively, are also run. If at the end of a simulation day, the CSF epidemic disappears, the scenario (SCE_m) is stopped and we start the simulation of the next scenario (SCE_{m+1}) .

At the end of the simulation (i.e., when the scenario (SCE_M) is finished), various outputs, described in Section 3.7, are generated and analyzed, especially those referring to risk evaluation.

A diagram summarizing CSM is presented in Figure 3.1.

3.2 Farm and transport of pigs inputs

We consider a study region containing $N_{fr} \in \mathbb{N}$ farms.

For each farm, identified as farm number i (also called, in order to simplify the notation, farm i), with $i = 1, \dots, N_{fr}$, the following data are given:

- $(X_i, Y_i) \in \mathbb{R}^2$: the geographical location.
- $N_i(0) \in \mathbb{N}$: the number of pigs at the first day of the simulation.
- $T_i \in \mathbb{N}$: the type of production of the farm. The model allows to distinguish three types of production: farrowing (young pigs), fattening (adult pigs) or farrow-to-finish (mixed pigs) [16].
- $INT_i \in \mathbb{N}$: its integrator group (i.e., groups of farms who share material and vehicles).
- $SDA_i \in \mathbb{N}$: its Sanitary Defense Association (SDA) group (i.e., groups of farms who share veterinaries).

Furthermore, the following data of all farm to farm pig shipments, occurring during the simulation time interval, are also provided:

- The number of pigs shipped.
- The date of shipment.
- The farms of origin and destination of the shipment.

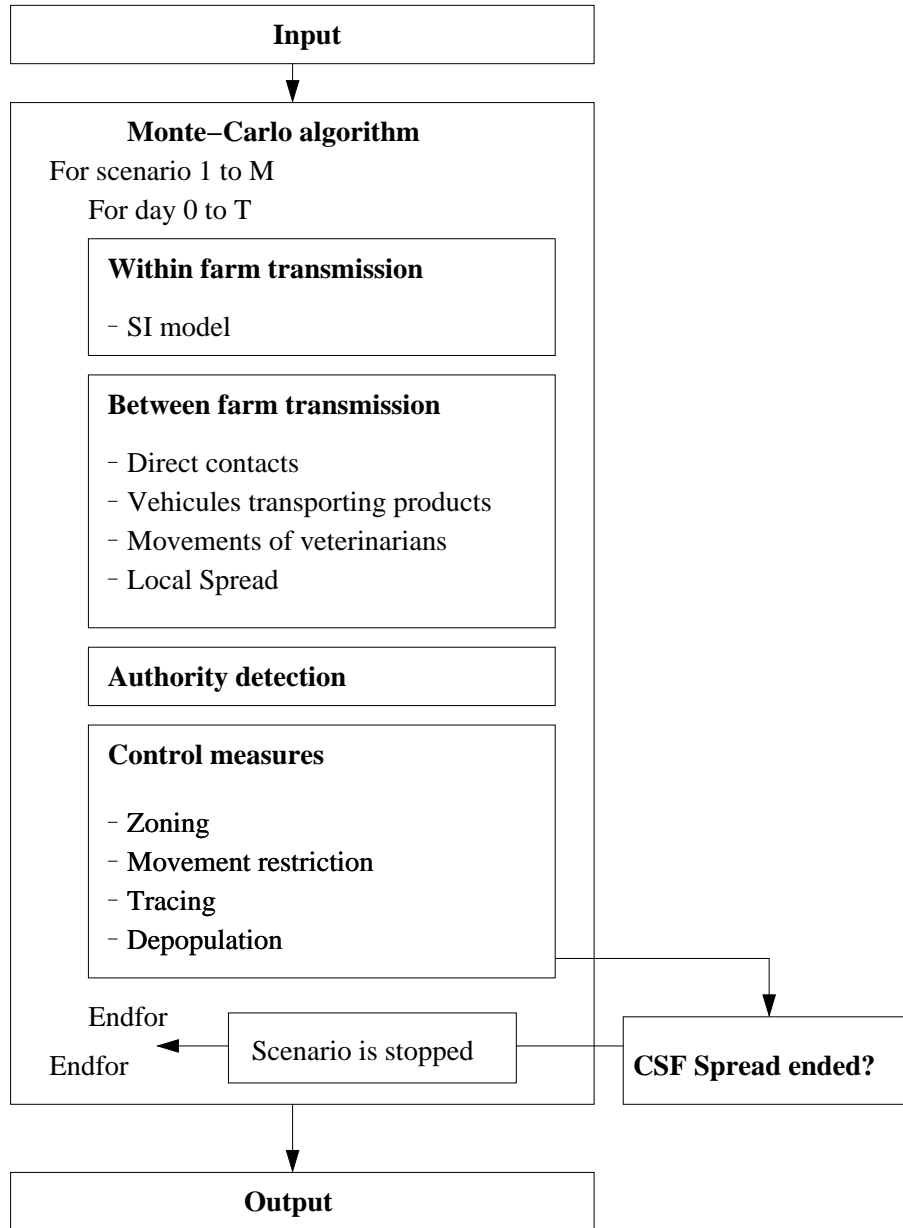


Figure 1: Diagram summarizing CSM presented in Section 3.1.

3.3 Within-farm CSFV spread

The daily CSFV spread within a particular farm i is modeled by using a discrete time stochastic Susceptible-Infected model [4, 16]. The pigs in this farm are characterized to be in one of those two states: 'Susceptible' or 'Infected', described in Section 2. In order to reduce the computational complexity of our model, the 'Infectious' and 'Clinical Signs' states are simulated only at the farm level (see Section 3.4 for more details). As the time period considered is inferior to one year, the natural pig mortality is also neglected.

Under those assumptions, the evolution of $S_{(p,i)}^c(t)$ and $I_{(p,i)}^c(t)$, the number of susceptible and infected pigs in farm i at time t respectively, are given (in a continuous version) by

$$\begin{cases} \frac{dS_{(p,i)}^c(t)}{dt} = -\beta_i \frac{S_{(p,i)}^c(t)I_{(p,i)}^c(t)}{S_{(p,i)}^c(t)+I_{(p,i)}^c(t)}, \\ \frac{dI_{(p,i)}^c(t)}{dt} = \beta_i \frac{S_{(p,i)}^c(t)I_{(p,i)}^c(t)}{S_{(p,i)}^c(t)+I_{(p,i)}^c(t)}, \end{cases} \quad (1)$$

where $\beta_i \in \mathbb{R}$ is the daily transmission parameter set to 0.656, 0.402 or 0.529 depending of the farm type T_i : farrowing, fattening, farrow-to-finish pig farms, respectively [16]. The evolution of the proportion of infected pigs considering (1) and a farm of 1000 pigs starting with 1 infected pig, in function of the farm type, is presented in Figure 2.

In order to obtain an integer value of infected and susceptible pigs and to introduce some randomness in (1) (the within-farm CSFV spread may be slightly different for each farm), but respecting its general behavior, we have considered the following daily discrete system version of (1) [16]

$$\begin{cases} S_{p,i}(t+1) = S_{p,i}(t) - \min(P(t), S_{p,i}(t)), \\ I_{p,i}(t+1) = I_{p,i}(t) + \min(P(t), S_{p,i}(t)), \end{cases} \quad (2)$$

where t corresponds to the day in the simulation and $P(t) \in \mathbb{N}$ follows a Poisson distribution with mean of $\beta_i \frac{S_{(p,i)}(t)I_{(p,i)}(t)}{S_{(p,i)}(t)+I_{(p,i)}(t)}$.

Here, to decrease the computational time needed by our model, this process is only performed at simulation day t for the farms such that $I_{p,i}(t) > 0$ and $S_{p,i}(t) > 0$.

3.4 Between-farm CSFV spread

CSFV spread between farms is modeled by using a spatial stochastic individual based model [6, 14]. In this model, farms are classified in one of these four states: 'Susceptible' (S_f), 'Infected' (I_f), 'Infectious' (T_f) and 'Clinical signs' (C_f). Those states are described in Section 2.

The daily transition from a particular farm state to the other state is modeled by considering direct contacts, indirect contacts and the natural evolution of the CSF presented in Section 2. Those transition processes are described in detail in Sections 3.4.1-3.4.3.

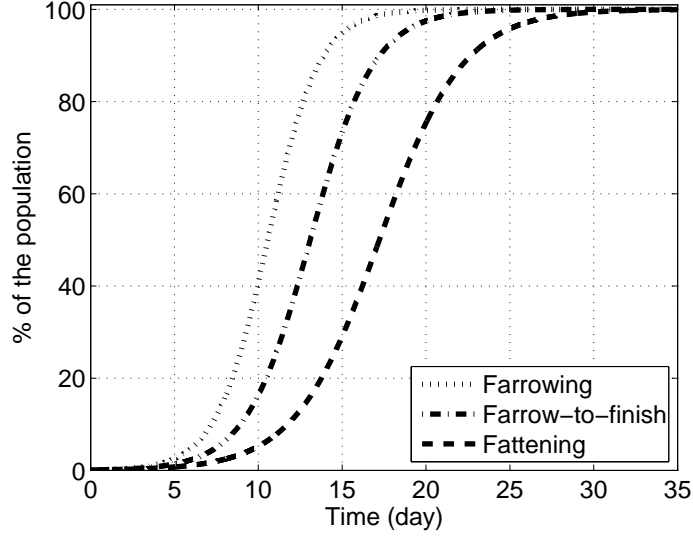


Figure 2: Evolution of the percentage of infected pigs obtained by considering (1) and a farm of 1000 pigs starting with 1 infected pig, in function of the farm type: farrowing, fattening and farrow-to-finish.

3.4.1 State transition due to direct contacts

CSFV spread by direct contacts is assumed to occur due to the movement of infected pigs between farms. The movements from farm to farm are simulated by using the data of the movements of pigs introduced in Section 3.2. Since the transport of pigs are similar from one year to another [13, 27, 21], we generate random movements, respecting the database behavior (with data from previous year), instead of using its exact movements.

More precisely, for each simulation day t , we simulate those movements by performing this process:

- We compute $SNM(t)$, the estimated number of movements occurring during simulation day t , by considering a Poisson distribution of rate $NM(t)$, where $NM(t) \in \mathbb{N}$ is the number of movements occurring at day t in our database.
- Then, for each simulated movement:
 - We select randomly a farm of origin of the movement $i \in [1, \dots, N_{fr}]$ and a farm of destination of the movement $j \in [1, \dots, N_{fr}]$, with $j \neq i$, by considering the discrete probability \mathbb{P}_M defined by:

$$\mathbb{P}_M((i, j) = (k, l)) = \frac{M_{\text{mov}}(k, l)}{\sum_{m=1}^{N_{fr}} \sum_{n=1}^{N_{fr}} M_{\text{mov}}(m, n)}, \quad (3)$$

where $k \in [1, \dots, N_{fr}]$, $l \in [1, \dots, N_{fr}]$, $k \neq l$ and $M_{\text{mov}}(k, l) \in \mathbb{R}$ is the number of movements from farm k to l in the database plus 10^{-6} (to take into account possible movements not occurring in our database).

- We compute $np_{(i,j)}(t) \in \mathbb{N}$, the number of pigs moved during this movement from farm i to farm j , by considering:

$$np_{(i,j)}(t) = \min \left\{ \text{Ceil}(\overline{np_{(i,j)}} \frac{S_{p,i}(t) + I_{p,i}(t)}{N_i(0)}), S_{p,i}(t) + I_{p,i}(t) \right\}, \quad (4)$$

where $\overline{np_{(i,j)}} \in \mathbb{R}$ is the mean number of pigs moved between those farms in our database and $\text{Ceil}(x) \in \mathbb{N}$ returns the nearest integers greater or equal to $x \in \mathbb{R}$. In case of no movements from farm i to farm j in the database, $\overline{np_{(i,j)}}$ is set to the mean number of moved pigs, considering all movements in the database.

- Finally, we move $np_{(i,j)}(t)$ pigs from the origin farm i to the destination farm j . Those pigs are selected randomly in $S_{p,i}(t)$ and $I_{p,i}(t)$. We denote by $np_{(i,j),S}(t) \in \mathbb{N}$ the number of susceptible pigs moved and by $np_{(i,j),I}(t) \in \mathbb{N}$ the number of infected pigs moved. Thus, the evolution of pigs in farm i and j are governed by

$$\begin{cases} S_{p,i}(t+1) = S_{p,i}(t) - np_{(i,j),S}(t), \\ I_{p,i}(t+1) = I_{p,i}(t) - np_{(i,j),I}(t), \\ S_{p,j}(t+1) = S_{p,j}(t) + np_{(i,j),S}(t), \\ I_{p,j}(t+1) = I_{p,j}(t) + np_{(i,j),I}(t). \end{cases} \quad (5)$$

In addition, if $np_{(i,j),I}(t) > 0$, the state of farm j is set to the state of farm i in the following cases:

- * The state of farm j is S_f or
- * The state of farm j is I_f and the state of farm i is T_f or C_f or
- * The state of farm j is T_f and the state of farm i is C_f .

In all other cases, the state of farm j remains unchanged.

3.4.2 State transition due to indirect contacts

CSFV spread by indirect contacts is assumed to occur by either movement of vehicles transporting pigs, movement of vehicles transporting products, movement of veterinarians or local spread (due to airborne spread, contact with contaminated neighborhood people and contaminated fomites), as specified in Section 2.

In paragraphs *A-D*, we describe in detail those four kinds of indirect contacts and the way they contribute to CSFV spread from farm to farm. Then, in paragraph *E*, we show how this spread affects the farm at the level of pig number and state.

A- Movements of vehicles transporting pigs:

We consider the same movements as the ones generated in Section 3.4.1. If the farm of origin of the transport is in the infectious state (i.e., in state either T_f or C_f), the truck transporting pigs is considered as infectious and has a probability to infect the farm of destination. Finally, we assume that the probability of CSFV infection in the farm of destination due at contact with the infectious vehicle is modeled by using a Bernoulli distribution with mean 0.011 [38].

B- Movements of vehicles transporting products:

Contacts with vehicles transporting products from farm to farm (also called 'integrator vehicles') are assumed to occur only among the farms belonging to the same integration group and with the following assumptions:

- The daily number of contacts with integrator vehicles per farm is assumed to be Poisson distributed with a rate of 0.4 [14].
- A vehicle can visit a maximum of $N_{INT} \in \mathbb{N}$ farms per day [13, 21, 27].
- A vehicle can only be infectious if, previously, it has visited an infectious farm [14, 38].
- The probability of CSFV infection in a farm per contact with an infectious integrator vehicle is modeled by using a Bernoulli distribution with mean 0.0068 [38].

Thus, for each simulation day, we build the routes of those integrator vehicles and simulate the way they spread CSFV by considering the following process:

For each integrator groups INT , we perform these steps:

- For each farm in INT , we compute the number of integrator vehicles visiting it by using a Poisson distribution with a rate of 0.4.
- Then, we list the farms that will be visited by one or more integrator vehicles and we arrange this list randomly (taking into account that a same farm cannot be visited two times consecutively). Thus, we obtained the visit order.
- Next, a first vehicle is sent to visit the first N_{INT} farms in the list following the visit order. Each N_{INT} -th farm, until the end of the list, we consider a new vehicle (non infectious) starting from the next farm in the list. During each simulated trip, a vehicle is considered infectious at the moment it visits an infectious farm and can infect other farm by considering a Bernoulli distribution with mean 0.0068.

C- Movements of veterinarians:

CSFV spread by contact with veterinarians visiting farms is assumed to occur only between farms belonging to the same Sanitary Defense Association (SDA) group.

The same process used above, for the movements of integrator vehicles, is applied to simulate those contacts with the following parameters:

- The daily number of veterinarian contacts per farm is assumed to be Poisson distributed with a rate of 0.3 [14].
- A veterinarian can visit a maximum of $N_{SDA} \in \mathbb{N}$ farms per day [13, 21, 27].
- A veterinarian can only be infectious if, previously, he has visited an infectious farm [14, 38].
- The probability of CSFV infection in a farm per contact with an infectious veterinarian is modeled by using a Bernoulli distribution with mean 0.0065 [38].

D- Local spread:

Local CSFV spread is assumed to occur to farms in the proximity of an infectious farms by indirect contacts such as airborne spread, contaminated neighborhood persons and contaminated fomites.

The daily probability of CSFV infection in a farm j due to local spread from an infectious farm i at simulation day t is modeled by considering a Bernoulli distribution with mean

$$\frac{I_{p,i}(t)}{N(0)} LSM(d(i, j)), \quad (6)$$

where $\overline{N(0)} = \frac{\sum_i N_i(0)}{N_{fr}}$ is the mean number of pigs per farms at day 0, $d(i, j)$ is the distance between farms i and j , and $LSM(x) \in [0, 1]$ is the mean daily probability of CSFV infection due to local spread between two farms at a distance of $x > 0$ (m) which is build by interpolating the data presented in Table 1 [14].

Table 1: Interpolation points used to compute $LSM(x)$ in function of the farms distance x (m).

Distance (m)	150	250	500	1000	2000
$LSM(x)$	0.014	0.009	0.0038	0.0019	0

E- New infection and state transition:

For each new CSFV infection occurring at farm j during the processes described in Section 3.4.2-A to 3.4.2-D, if $S_{p,j}(t) \geq 1$, we infect one new pig in farm j by considering:

$$\begin{cases} S_{p,j}(t+1) = S_{p,j}(t) - 1, \\ I_{p,j}(t+1) = I_{p,j}(t) + 1. \end{cases} \quad (7)$$

Furthermore, if the state of farm j is S_f , we change it to I_f .

3.4.3 State transition due to CSF natural evolution

According to the characteristics of the CSF described in Section 2, we consider the following changes in the farm state:

- Transition from I_f to T_f : when a farm reach the state I_f , it will pass at state T_f after a 'latent' period that follows a Poisson distribution with mean of 7 days [14].
- Transition from T_f to C_f : when a farm reach the state T_f , it will pass at state C_f after an 'incubation' period that follows a Poisson distribution with mean of 21 days [14].

3.5 Contaminated farm detection

As specified in Section 2, a contaminated farm is generally detected by observation of the clinical signs of its pigs (i.e., the farm is in state C_f) [18]. This detection is simulated differently before and after the detection of the first contaminated farm (i.e., the index case):

- Before detection of the index case: For each farm in the state C_f , the probability of detection per day is modeled by using a Bernoulli distribution with mean 0.03 [14].
- After detection of the index case: As the awareness of the farmers increase, the daily probability of detection of a farm in the state C_f is increased and is simulated by considering a Bernoulli distribution with mean 0.06 [14].

Furthermore, a contaminated farm can be also detected due to the control measures presented in Sections 3.6.1 and 3.6.4.

3.6 Control measures

In this Section, we will describe the control measures implemented in our model, and introduced in Section 2.

3.6.1 Zoning

A 'control' (<3 km radius) and 'surveillance' (>3 and <10 km radius) zones are defined around detected farms.

A movement restriction (i.e., movements leaving or entering in considered farms) of $N_{ZC} \in \mathbb{N}$ days is applied to farms in a control zone and of $N_{ZS} \in \mathbb{N}$ days for farm in a surveillance zone. In both cases, movements of pigs, movements of veterinarians and movements of integrator vehicles are randomly reduced by considering a Bernoulli distribution with mean $P_{ZA} \in [0, 1]$, $P_{ZV} \in [0, 1]$ and $P_{ZI} \in [0, 1]$, respectively [13, 21, 27]. Overlapping of the movement restrictions of control and surveillance zones is allowed (i.e, if a farm has an active movement restriction, we add the days of the 'new' restriction to those of the 'old' restriction).

Furthermore, we apply another surveillance process to the farms within those radius, in addition to the one described in Section 3.5. The daily probability detection of a farm j in the state C_f due to this surveillance is modeled by considering

- a Bernoulli distribution with mean $P_{ZC} \frac{I_{p,j}(t)}{S_{p,j}(t) + I_{p,j}(t)}$ if farm j is within a control zone,
- a Bernoulli distribution with mean $P_{ZS} \frac{I_{p,j}(t)}{S_{p,j}(t) + I_{p,j}(t)}$ if farm j is within a surveillance zone and is not within a control zone.

In both cases, the probability of detection is assumed to be dependent of the proportion of infected animals and has a maximum value estimated to $P_{ZC} \in [0, 1]$ and $P_{ZS} \in [0, 1]$ (assuming possible failures in the surveillance process), in control and surveillance zones respectively [13, 21, 27].

3.6.2 Movement restrictions

A drastic restriction of movements is applied to detected farms. Restrictions of transport of animals, integrator vehicle movements and veterinarian movements in the detected farms are assumed to be Bernoulli distributed with a mean of $P_{MA} \in [0, 1]$, $P_{MI} \in [0, 1]$ and $P_{MV} \in [0, 1]$, respectively. Furthermore, after each detection, a general movement restriction (i.e., considering all movement types) is applied to all farms for a period of $N_{RF} \in \mathbb{N}$ days following a Bernoulli distribution with a mean of $P_{MR} \in [0, 1]$ [13, 21, 27].

3.6.3 Depopulation

The depopulation (i.e., the sacrifice of all animals) of detected farms is assumed to occur after a random time period generated using data provided by the Table 2 [9]. The maximum number of farms to be depopulated per day is assumed to follow a Poisson distribution of $N_{DF} \in \mathbb{N}$. If this limit is reached, the farm will be depopulated the day after. A depopulated farm will not be considered by the model until its repopulation. The repopulation of the farm occurs after

a period following a Poisson distribution of $N_{DR} \in \mathbb{N}$ days. The number of susceptible pigs used to repopulate the farm i is $N_i(0)$ and the farm state is set to S_f [13, 21, 27].

Days	0	1	2	3	4	5	6	7	8
Prob.	0,11	0,58	0,2	0,06	0,04	0,004	0,003	0,0015	0,0015

Table 2: Probability distribution (Prob.) of the number of days to wait before depopulating a farm.

3.6.4 Tracing

The objective of tracing is to identify infectious contacts which may have introduced CSFV into a detected farm or spread CSFV to other farms. We include tracing of all contacts of a detected farm (i.e., farms sending or receiving animals, sharing veterinarians or sharing integrator vehicles) occurring $N_{TF} \in \mathbb{N}$ days before the detection. However, due to failure in the administrative system (error in database, lack of personnel, etc.) tracing all the contacts is not always possible. Thus, the probability of tracing a contact due to animal transport, integrator vehicle or veterinarian movement is assumed to be Bernoulli distributed with mean $P_{TA} \in [0, 1]$, $P_{TI} \in [0, 1]$ and $P_{TV} \in [0, 1]$, respectively [13, 21, 27]. Finally, the probability of detecting a contaminated traced farm follows a Bernoulli distribution with mean 0.95 [14].

3.7 Model outputs

At the end of the M scenarios (SCE_m), $m = 1, 2, \dots, M$, many kinds of outputs can be obtained. For instance, here, we consider the following outputs:

- The number of infected farms.
- The duration of the epidemic (in days).
- The percentage of infections due to each direct and indirect contacts.
- The number of farms in a control or surveillance zones.
- The number of traced farms.
- The percentage of detection of infected farms due to clinical signs, zoning or tracing after the detection of the index case.

For all those quantities, we compute the mean value considering all scenarios and the minimum and maximum values of the 95% (or any other percentage) prediction interval (denoted by 95%PI) [11, 38].

Furthermore, we compute the following risk values:

- The risk of CSFV introduction in a farm i (denoted by RI_i): It is defined as the number of times that farm i became infected considering all scenarios.
- Basic reproduction ratio of a farm i (denoted by $R0_i$): It is defined as the number of times that farm i infects another farm in the susceptible state considering all scenarios [1, 2]. Basically, it represents the risk that farm i infect other ones.

We can obtain the geographical distribution of RI and $R0$ in the considered region by interpolating the respective $R0_i$ and RI_i values obtained for each farm i .

All those parameters allow to have a quantification of the CSFV spread.

4 Numerical Experiments

4.1 Considered experiments

In order to illustrate the CSM performances, we have considered the province of Segovia (one of the most important areas of pig production in Spain) which was affected by the 1997-1998 CSF-epidemic [13, 27]. During 2008, Segovia had approximately $N_{fr} = 2235$ pig farms, 1403800 pigs, and there were 10046 pig movements. Real data, for the inputs described in Section 3.2, have been provided by the "Regional Government of Castilla and Leon" and the Spanish "Ministry of the Environment and Rural and Marine Affairs" [13, 21, 27]. Furthermore, the following model parameters, well suited for the province of Segovia, have been considered [13, 21]:

$$\begin{array}{llll}
N_{ZC}=51, & N_{ZS}=40, & P_{ZA}=0.95, & P_{ZV}=0.90, \\
P_{ZI}=0.70, & N_{INT}=4, & N_{SDA}=3, & P_{ZC}=0.98, \\
P_{ZS}=0.95, & P_{MA}=0.99, & P_{MI}=0.95, & P_{MV}=0.80, \\
P_{MR}=0.40, & N_{RF}=90, & N_{DF}=20, & N_{DR}=90, \\
N_{TF}=60, & P_{TA}=0.99, & P_{TI}=0.70, & P_{TV}=0.40.
\end{array}$$

A graphical representation of the locations of the province of Segovia and the considered pig farms is shown in Figure 3.

We have considered two experiments:

- In the first one, we do not consider the control measures and we run the model with $T = 200$ days. This case is denoted by **NM** (No Measure). The interest of this experience is to evaluate the principal way of CSFV spread.
- In the second one, all control measures described previously are activated and the model is running until the end of the CSF epidemic. This case is denoted by **WM** (With Measures). In this experiment, which is more realistic than the previous one, we are interested in evaluating the magnitude of the epidemic and the efficiency of the control measures.

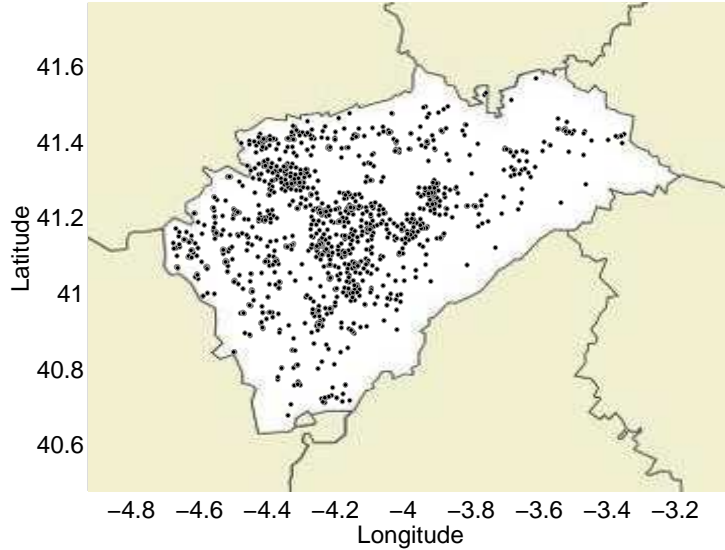


Figure 3: Coordinates and boundaries of the Region of Segovia (in white). Location of considered pig farms is represented by black spots (\bullet).

In both cases, we set $M = 1000$ scenarios.

In order to perform those experiments, we have used a MatLab implementation of CSM, called *Be-FAST* (Between-Farm-Animal Spatial Transmission) [22], on a Pentium 4 of 3.4Ghz with 2Gb. It needed around 15000 seconds for the **NM** case and around 20000 seconds for the **WM** case.

The results are presented in Section 4.2.

4.2 Results

Some outputs obtained for the **NM** and **WM** cases are shown in Tables 3 and 4, respectively. For both experiments, we present in Figure 4 the R_0 and RI interpolated maps of the considered region.

As we can observe from Table 3, the principal cause of infection is, in this order, the local spread, integrator vehicles, veterinarians, transport of pigs and transport vehicles. Those values are consistent with studies referring to real CSFV outbreaks [5, 37]. This order is also verified in the **WM** experiments. In addition, we can see in Figures 3 and 4 that the R_0 and RI maps are similar and, in the **NM** case, their high risk values are concentrated in the high density farm areas, which is consistent with experimental results presented in [3].

In Table 4, we can note that the main way to detect an infected farm is the observation of clinical signs. However, we can observe that the tracing

Quantity	Mean	Min.	Max.
Number of Infected farms	32	1	138
% of infections due to local spread	62	0	100
% of infections due to integrator vehicles	21	0	100
% of infections due to veterinarians	10	0	86
% of infections due to transport of pigs	7	0	50
% of infections due to vehicles transporting pigs	0.1	0	1

Table 3: Results obtained considering the **NM** case. For each quantity, we present its mean value considering all scenarios and the minimum (Min.) and maximum (Max.) values of its 95%PI.

Quantity	Mean	Min.	Max.
Number of Infected farms	3	1	17
Duration of the epidemic in days	63	23	177
Number of farm in a zone	151	0	579
Number of traced farm	98	0	1378
% of detections due to clinical signs	60	20	100
% of detections due to tracing	32	0	75
% of detections due to zoning	8	0	50

Table 4: Results obtained considering the **WM** cases. For each quantity, we present its mean value considering all scenarios and the minimum (Min.) and maximum (Max.) values of its 95%PI.

activity helps to identify around 32% of the infected farms. From a general point of view, control measures help to reduce the magnitude of the CSF epidemic to a mean value of 3 infected farms and a mean duration of 63 days. Those results are consistent with other experiments done by considering the individual based model presented in [14, 15] and a study region with characteristics similar to Segovia [15]. Moreover, the $R0$ and RI risk values decrease drastically by applying those control measures. This can be observed in Figure 4, where the high risk zones (i.e., values ≥ 9) have an enormous reduction when comparing the **NM** and **WM** results. Those remaining high risk zones also indicate that the application of the considered control measures is not able to eradicate completely the risk of CSF epidemic. An interesting future problem could be to use this model to test the efficiency of possible alternative preventive measures.

An interpretation and analysis of these results, from the point of view of a veterinarian specialist is available in [22].

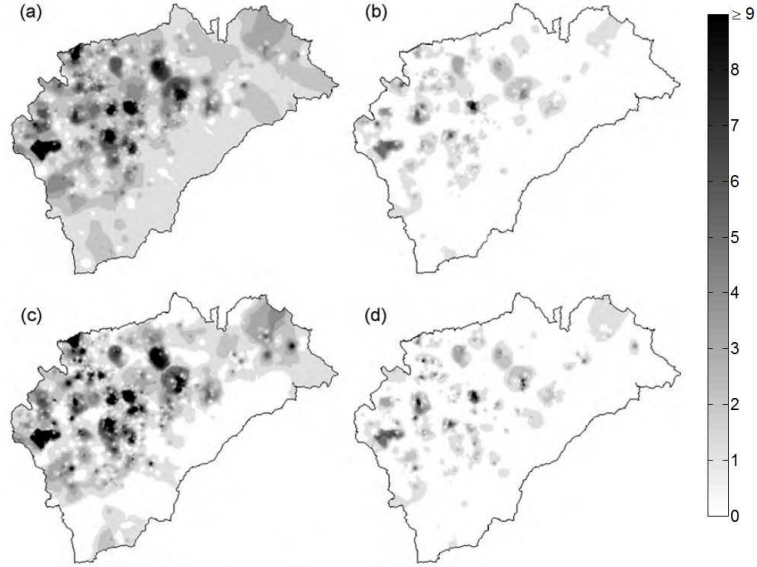


Figure 4: (**TOP**) *RI* and (**BOTTOM**) *R0* interpolated maps for (**LEFT**) **NM** and (**RIGHT**) **WM** cases.

From a modeling point of view, the main improvement of the model presented here, with respect to other already existing models [14, 35], is the use of a realistic database instead of random data, allowing us to obtain a realistic repartition of the CSF risk zones. Furthermore, the hybridization between a Susceptible-Infected model with an individual based model, allows to consider model parameters that take into account the pig population size and the proportion of infected pigs. Thus, the model is able to reproduce real CSF data, showing that the CSFV spreads faster in zones of high population density or with a high proportion of infected pigs [8, 13, 26, 30].

4.3 Model sensitivity analysis

In order to test the robustness of our model with respect to its parameters, we have performed a brief sensitivity analysis in the **WM** case by perturbing randomly all the parameters with a maximum amplitude of 10%. Results are robust with a change inferior to 10%. A more exhaustive sensitivity analysis is performed in [23].

5 Conclusions

During this work, we have introduced and described a model for the study of CSFV spread into a region. The principal originality of this model is that it combines a Susceptible-Infected model, for the within-farm spread process, with an Individual Based Model, for the between-farm spread process. Another important model characteristic, is the use of a complete and realistic database (for instance, transport data). This model has given preliminary results consistent with other works and presents interesting and novel characteristics with respect to them.

Next steps would be to present a more complete model sensitivity analysis and validation by considering the CSFV outbreaks of Segovia occurring in 1997-98 (this work is currently in preparation in [23]), and to study the application of the model to risk management in order to reduce the remaining high risk zones previously identified.

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